detecting the presence or absence of a mutation associated with hypertrophic cardiomyopathy in the amplified product thereby facilitating the diagnosis of hypertrophic cardiomyopathy.

2. The method of claim 1 wherein the hypertrophic cardiomyopathy is familial hypertrophic cardiomyopathy.

3. The method of claim 1 wherein the hypertrophic cardiomyopathy is sporadic hypertrophic cardiomyopathy.

4. The method of claim 2 wherein the mutation associated with hypertrophic cardiomyopathy is a point mutation.

5. The method of claim 4 wherein the point mutation is a missense mutation.

6. (Amended) The method of claim 1 wherein the mutation associated with hypertrophic cardiomyopathy is [a small alteration in the amplified DNA] of a size less than the amplified product.

7. (Amended) The method of claim 1 wherein the ß cardiac myosin heavy-chain DNA is cDNA [reversed] reverse transcribed from RNA.

8. The method of claim 7 wherein the RNA is obtained from nucleated blood cells.

9. The method of claim 1 wherein the presence or absence of the mutation associated with hypertrophic cardiomyopathy is detected by combining the amplified product with an RNA probe completely hybridizable to normal ß cardiac myosin heavy-chain DNA forming a hybrid double strand having an RNA and DNA strand, the hybrid double strand having an unhybridized portion of the RNA strand at any portion corresponding to a hypertrophic cardiomyopathy associated mutation in the DNA strand; and

detecting the presence or absence of an unhybridized portion of the RNA strand as an indication of the presence or absence of a hypertrophic cardiomyopathy associated mutation in the corresponding portion of the DNA strand.

10. The method of claim 2 wherein the presence or absence of the mutation associated with familial hypertrophic cardiomyopathy is detected by combining the amplified product with an RNA probe completely hybridizable to normal ß cardiac myosin heavy-chain DNA forming a hybrid double strand having an RNA and DNA strand, the hybrid double strand having an unhybridized ribonucleotide of the RNA strand at any portion corresponding to a familial hypertrophic cardiomyopathy associated point mutation in the DNA strand;

contacting the hybrid double strand with an agent capable of digesting an unhybridized portion of the RNA strand; and

detecting the presence or absence of an unhybridized ribonucleotide of the RNA strand as an indication of the presence or absence of a familial hypertrophic cardiomyopathy associated point mutation in the corresponding deoxyribonucleotide of the DNA strand.

11. The method of claim 1 wherein the ß cardiac myosin heavy-chain DNA is amplified using a polymerase chain reaction.

12. (Amended) The method of claim 11 wherein the polymerase chain reaction is [a nested polymerase chain reaction] performed with nested primers.

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13. (Amended) A method for diagnosing familial hypertrophic cardiomyopathy comprising:

obtaining a sample of ß cardiac myosin heavy-chain DNA derived from a subject being tested for hypertrophic cardiomyopathy; and

diagnosing the subject for familial hypertrophic cardiomyopathy by detecting the presence or absence of a familial hypertrophic [cardiomyopathy-causing] cardiomyopathy-associated point mutation in the ß cardiac myosin heavy-chain DNA as an indication of [the disease] familial hypertrophic cardiomyopathy.

14. The method of claim 13 wherein the ß cardiac myosin heavy-chain DNA is cDNA reverse transcribed from RNA obtained from the subject's nucleated blood cells.

15. The method of claim 13 further comprising amplifying the ß cardiac myosin heavy-chain DNA prior to the diagnosis step.

16. The method of claim 15 wherein an exon suspected of containing the familial hypertrophic cardiomyopathy-causing point mutation is selectively amplified.

17. The method of claim 13 wherein the point mutation is selected from the group consisting of Arg249Gln, Arg403Gln, Arg453Cys, Gly584Arg, Val606Met, Glu924Lys, and Glu949Lys.

18. (Amended) A non-invasive method for diagnosing hypertrophic cardiomyopathy, comprising:

obtaining a [blood] cell sample from a subject being tested for hypertrophic cardiomyopathy;

isolating ß cardiac myosin heavy-chain RNA from [the blood] said sample; and

diagnosing the subject for hypertrophic cardiomyopathy by detecting the presence or absence of a familial hypertrophic cardiomyopathy-associated mutation in the RNA as an indication of [the disease] hypertrophic cardiomyopathy.

19. The method of claim 18 wherein the presence or absence of a hypertrophic cardiomyopathy-associated mutation in the RNA is detected by preparing ß cardiac myosin heavy-chain cDNA from the RNA forming ß cardiac myosin heavy-chain DNA and detecting mutations in the DNA as being indicative of mutations in the RNA.

20. The method of claim 18 further comprising amplifying the ß cardiac myosin heavy-chain DNA prior to detecting a hypertrophic cardiomyopathy-associated mutation in the DNA.

21. The method of claim 18 wherein the hypertrophic cardiomyopathy is familial hypertrophic cardiomyopathy.

22. The method of claim 18 wherein the hypertrophic cardiomyopathy is sporadic hypertrophic cardiomyopathy.

23. The method of claim 18 further comprising evaluating the subject for clinical symptoms associated with familial hypertrophic cardiomyopathy.

24. (Amended) A method for [detecting the presence or absence of] identifying a [disease] hypertrophic cardiomyopathy-associated mutation in a DNA sequence present in a genomic DNA sample, comprising:

amplifying [a] said DNA sequence, wherein said sequence is suspected of containing a [disease] hypertrophic cardiomyopathy-associated mutation forming an amplified product;

[combining the] hybridizing said amplified product with an RNA probe, wherein said RNA probe is completely hybridizable to a normal DNA sequence not containing said mutation [associated with the disease] forming [a hybrid double strand having] an RNA: [and] amplified DNA [strand] duplex, [the hybrid double strand having an unhybridized] wherein a portion of the RNA [strand at a portion corresponding] is not hybridized to a [disease-associated mutation in] corresponding portion of the amplified DNA [strand]; and

detecting [the presence or absence of an] said unhybridized portion of the RNA [strand] , wherein said detecting identifies [as an indication of] the presence [or absence] of a [disease] hypertrophic cardiomyopathy-associated mutation in the corresponding portion of the DNA [strand].

25. (Amended) The method of claim 24 wherein the [disease] hypertrophic cardiomyopathy-associated mutation is a point mutation in the DNA strand.

26. (Amended) The method of claim 24 wherein the [disease] hypertrophic cardiomyopathy-associated mutation [is a small alteration in the DNA strand] is selected from the group consisting of additions, deletions, substitutions of one or more nucleotides, and combinations thereof.

27. (Amended) The method of claim 24 wherein [the presence or absence of an unhybridized portion of the RNA strand is detected by] said detecting comprises the steps of:

contacting [the hybrid double strand] said duplex with an agent [capable of digesting an] that digests the unhybridized RNA portion(s) of [the RNA strand] said duplex,

denaturing [the hybrid double strand], said digested duplex,

separating the denatured RNA fragments by size, and

comparing the separated fragments [of RNA resulting from portions of the RNA strand being digested by the agent] to RNA fragments representative of normal RNA.

28. (Amended) The method of claim 24 further comprising sequencing a portion of DNA corresponding to an unhybridized portion of the RNA strand to identify the sequence of a [disease] hypertrophic cardiomyopathy-associated mutation.

29. (Amended) The method of claim 24 wherein detecting [the presence or absence of] more than one unhybridized portion of the RNA [strand are detected as an indication of] identifies the presence [or absence] of more than one [disease] hypertrophic cardiomyopathy-associated mutation in the corresponding portions of the DNA [strand].

30. (Amended) The method of claim 24 [whereins] wherein the DNA sequence suspected of containing a [disease] hypertrophic cardiomyopathy-associated mutation is amplified using a polymerase chain reaction.

31. (Cancelled) The method of claim 30 wherein the polymerase chain reaction is a nested polymerase chain reaction.

32. A method for determining the estimated life expectancy of a person having familial hypertrophic cardiomyopathy, comprising:

obtaining ß cardiac myosin DNA derived from a subject having familial hypertrophic cardiomyopathy;

detecting a familial hypertrophic cardiomyopathy-causing point mutation in the ß cardiac myosin DNA;

classifying the type of familial hypertrophic cardiomyopathy-causing point mutation; and

estimating the life expectancy of the subject using a Kaplan-Meier curve for the classified type of familial hypertrophic cardiomyopathy-causing point mutation.

33. (Amended) A kit useful for facilitating the diagnosis of [diagnosing] hypertrophic cardiomyopathy, comprising:

a first container holding an RNA probe completely hybridizable to the ß cardiac myosin heavy chain DNA; [and]

a second container holding primers useful for amplifying ß cardiac myosin heavy-chain DNA; and

instructions for using the components of the kit to detect the presence or absence of hypertrophic cardiomyopathy-associated mutations in amplified ß cardiac myosin heavy-chain DNA for facilitating the diagnosis of hypertrophic cardiomyopathy.

34. A kit of claim 33 further comprising a third container holding an agent for digesting unhybridized RNA.

35. ~~(Cancelled)~~ The kit of claim 33 further comprising instructions for using the components of the kit to detect the presence or absence of hypertrophic cardiomyopathy-associated point mutations in amplified ß cardiac myosin heavy-chain DNA.

36. (Amended) An isolated RNA probe comprising ribonucleotides arranged in a sequence which is complementary to at least a portion of ß-cardiac myosin heavy-chain DNA, said probe useful for facilitating the diagnosis of hypertrophic cardiomyopathy by being arranged for use in detecting a hypertrophic cardiomyopathy-associated mutation.

37. (Amended) A set of DNA oligonucleotide primers for amplifying ß-cardiac myosin heavy-chain DNA comprising, at least two oligonucleotides [capable of amplifying] which amplify ß-cardiac myosin heavy-chain DNA, said set of oligonucleotide primers being useful for facilitating the diagnosis of hypertrophic cardiomyopathy by being useful in the detection of a hypertrophic cardiomyopathy-associated mutation.

38. (Amended) The set of primers of claim 37 having at least four oligonucleotides.

39. (New) The oligonucleotide primers of claim 37, said primers comprising at least two oligonucleotides which amplify β-cardiac myosin heavy-chain DNA wherein the oligonucleotides are selected from the group consisting of:

5' CAAGGATCGCTACGGCTCCTGGAT 3' (SEQ ID NO:1),

5' GCGGATCCAGGTAGGCAGACTTGTCAGCCT 3' (SEQ ID NO: 2),

5' ATGCCAACCCTGCTCTGGAGGCCT 3' (SEQ ID NO: 3),

5' CTTCATGTTTCCAAAGTGCATGAT 3' (SEQ ID NO: 4),

5' CTGGGCTTCACTTCAGAGGAGAAAA 3' (SEQ ID NO: 5),

5' GCGGTACCCCAGCAGCCCGGCCTTGAAGAA 3' (SEQ ID NO: 6),

5' GGGAATTCGCGGAGCCAGACGGCACTGAAG 3' (SEQ ID NO: 7),

5' CCCTCCTTCTTGTACTCCTCCTGCTC 3' (SEQ ID NO: 8),

5' CAACTCATCACCACTCTCTTCCATC 3' (SEQ ID NO: 9), and

5' GCTGAGCCTAGCAGATTCATGGCAC 3' (SEQ ID NO: 10).

40. (New) The method of claim 1 wherein said hypertrophic cardiomyopathy-associated mutations are selected from the group consisting of G832A; C1443T; G1836C; G1902A; G2856A; and G2931A.

41. (New) A method according to claim 1 further comprising detecting the presence of more than one target sequence in said DNA.

42. (New) A method according to claim 40 wherein said more than one target sequence is a hypertrophic cardiomyopathy-associated mutation selected from the group consisting of G832A; G1294A; C1443T; G1836C; G1902A; G2856A; and G2931A.

43. (New) A method for detecting the presence of a target sequence in genomic DNA, wherein said target sequence is a member of a group of hypertrophic cardiomyopathy-associated mutations, wherein individual members of said group are located within different exons of the human β cardiac myosin gene, said method comprising:

amplifying one or more defined sequences of β cardiac myosin heavy-chain DNA present in said DNA;

identifying the products of said amplification; and

detecting the presence of at least one target sequence in said DNA.

REMARKS

Claims 1-30 and 31-43 are pending in the present application. Claims 39-43 have been added. Claim 31 has been cancelled. The above-noted claims have been amended. Cancellation of and/or amendment to any of the claims should in no way be construed as an acquiescence to any of the Examiner's rejections. The cancellation of and/or amendment to the claims are being made solely to expedite prosecution of the present application. Applicants reserve the option to further prosecute the same or similar claims in the instant or in a subsequent patent application.

Applicants have amended the specification to refer to all sequences embedded in the text or the claims by an identifier such as "SEQ ID NO" and is submitting a separate statement regarding the sequence listing for the purpose of complying with 37 C.F.R. §1.821.